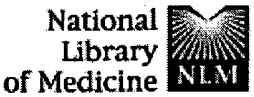
(FILE 'HOME' ENTERED AT 15:41:15 ON 17 AUG 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 15:43:02 ON 17 AUG 2004

L1	651	S PYRROLIDINOL
L2	97	S L1 AND PYRROLIDINONE
L3	4	S L2 AND MICROCOCCUS
L4	4	DUP REM L3 (0 DUPLICATES REMOVED)
L5	6138	S MICROCOCCUS (2N) LUTEUS
L6	246	S L5 AND (REDUCTASE OR REDUCTION)
L7	24	S L5 (10N) (REDUCTASE OR REDUCTION)
L8	21	DUP REM L7 (3 DUPLICATES REMOVED)
L9	35	S L2 AND (REDUCTION OR ASYMETRICALLY)
L10	33	DUP REM L9 (2 DUPLICATES REMOVED)





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- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#14	Search **nadph pyrrolidinone** Limits: **Publication Date to 1999**	11:25:08	62
#13	Search **nadph carbonyl reductase micrococcus** Limits: **Publication Date to 1999**	10:58:07	0
#11	Search **nadph carbonyl reductase asymmetric** Limits: **Publication Date to 1999**	10:57:15	1
#9	Search **nadph carbonyl reductase pyrrolidinone** Limits: **Publication Date to 1999**	10:56:50	0
#8	Search **nadph carbonyl reductase** Field: **All Fields,** Limits: **Publication Date to 1999**	10:56:32	135
#7	Search **nadph carbonyl reductase** Field: **All Fields,** Limits: **Publication Date to 2000**	10:56:17	147
#6	Search **nadph carbonyl reductase**	10:56:04	200
#5	Search **micrococcus luteus nadph**	10:55:40	7
#3	Search **micrococcus luteus reductase carbonyl**	10:55:16	1
#2	Search **micrococcus luteus reductase**	10:55:07	36
#1	Search **micrococcus luteus**	10:55:00	1030

Clear History

h cb hg e e e fcg b e

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BD141394
LOCUS       BD141394                 834 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel carbonyl reductase, gene thereof and method of using the
            same.
ACCESSION   BD141394
VERSION     BD141394.1  GI:23236339
KEYWORDS    WO 0210399-A/1.
SOURCE      Micrococcus luteus
  ORGANISM  Micrococcus luteus
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micrococcineae; Micrococcaceae; Micrococcus.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   Kizaki,N., Yasohara,Y. and Hasegawa,J.
  TITLE     Novel carbonyl reductase, gene thereof and method of using the same
  JOURNAL   Patent: WO 0210399-A 1 07-FEB-2002;
            KANEKA CORP,NORIYUKI KIZAKI,YOSHIHIKO YASOHARA,JUNZO HASEGAWA
COMMENT     OS   Micrococcus luteus
            PN   WO 0210399-A/1
            PD   07-FEB-2002
            PF   01-AUG-2001 WO 2001JP006619
            PR   01-AUG-2000 JP 00P   232756
            PI   NORIYUKI KIZAKI,YOSHIHIKO YASOHARA,JUNZO HASEGAWA PC
            C12N15/53,C12N9/02,C12N1/21,C12P17/10//(C12N15/53,C12R1:265) CC
            Novel carbonyl reductase, gene thereof and
            method of using the
            CC           same.
            FH   Key             Location/Qualifiers
            FT   source          1. .834
            FT                   /organism='Micrococcus luteus'.
FEATURES             Location/Qualifiers
     source          1. .834
                     /organism="Micrococcus luteus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1270"
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 5.8e-88;
  Matches  834;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        108 ATGCGACGGATGACGCTGCCGAGTGGGGAGTCCATCCCTGTGCTGGGCCAGGGCACCTGG 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCGACGGATGACGCTGCCGAGTGGGGAGTCCATCCCTGTGCTGGGCCAGGGCACCTGG 60

Qy        168 GGCTGGGGTGAGGACCCCGGCCGCCGCGGCGACGAGGTCGCCGCGCTGCACGCCGGCCTC 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCTGGGGTGAGGACCCCGGCCGCCGCGGCGACGAGGTCGCCGCGCTGCACGCCGGCCTC 120

Qy        228 GAGCTGGGCATGACGCTGGTCGACACCGCCGAGATGTACGCCGACGGCGGTGCGGAGGAG 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGCTGGGCATGACGCTGGTCGACACCGCCGAGATGTACGCCGACGGCGGTGCGGAGGAG 180

Qy        288 GTGGCTGGTGAAGCATTGGCGGGTCGCCGCGACGAGGCGTTCGTGGTCAGCAAGGTCATG 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGCTGGTGAAGCATTGGCGGGTCGCCGCGACGAGGCGTTCGTGGTCAGCAAGGTCATG 240
```

```
Qy        348 CCGTCCCACGCCTCCCGTTCCGGCACGATCGCGGCCTGCGAACGCAGCCTGAAACGCCTG 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGTCCCACGCCTCCCGTTCCGGCACGATCGCGGCCTGCGAACGCAGCCTGAAACGCCTG 300

Qy        408 GGCACCGATCGGATCGACCTCTACCTGCTGCACTGGCAGGGCAGGTACCCGCTGCAGGAC 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCACCGATCGGATCGACCTCTACCTGCTGCACTGGCAGGGCAGGTACCCGCTGCAGGAC 360

Qy        468 ACCGTCGCGGCCTTCCACCAGCTCGTCGAGGACGGGAAAATCCGATACTGGGGCGTCAGC 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCGTCGCGGCCTTCCACCAGCTCGTCGAGGACGGGAAAATCCGATACTGGGGCGTCAGC 420

Qy        528 AACTTCGACCACCGGGCCCTCGCCGAGCTGCAGGACGTGCCGGGCACCAGCGGGCTGACC 587
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTTCGACCACCGGGCCCTCGCCGAGCTGCAGGACGTGCCGGGCACCAGCGGGCTGACC 480

Qy        588 ACGGATCAGGTGCTGTACAACCTGTCGCGGCGAGGACCGGAGTACGACCTGCTGCCGTGG 647
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACGGATCAGGTGCTGTACAACCTGTCGCGGCGAGGACCGGAGTACGACCTGCTGCCGTGG 540

Qy        648 TGCGCCGACCACCAGCTGCCGGTCATGGCGTACTCGCCGATCGAGCAGGGCCGCATCCTT 707
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGCCGACCACCAGCTGCCGGTCATGGCGTACTCGCCGATCGAGCAGGGCCGCATCCTT 600

Qy        708 GACGACACGACGCTGAACGACGTCGCGGCCCGTCACAGCGTCAGCCCCGCGGCGGCGGCC 767
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACGACACGACGCTGAACGACGTCGCGGCCCGTCACAGCGTCAGCCCCGCGGCGGCGGCC 660

Qy        768 CTTGCCTGGGTGCTGCGCCGCGACTCGCTCTGCACGATCCCCAAGGCGAGCAGCCCGCAG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTGCCTGGGTGCTGCGCCGCGACTCGCTCTGCACGATCCCCAAGGCGAGCAGCCCGCAG 720

Qy        828 CACGTGCGCGACAACGCCACAGCACTGGACGTGGAGCTGACCCGCGAAGACCTGGATGCT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CACGTGCGCGACAACGCCACAGCACTGGACGTGGAGCTGACCCGCGAAGACCTGGATGCT 780

Qy        888 CTGGACCGTGCGTTTCCGCCCCCGAGCGGACCGCGACCACTGGAAATGCTGTGA 941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGGACCGTGCGTTTCCGCCCCCGAGCGGACCGCGACCACTGGAAATGCTGTGA 834
```

RESULT 2
ABU22187
ID ABU22187 standard; protein; 281 AA.
XX
AC ABU22187;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #7714.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Burkholderia mallei.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA26057.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 50111; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 281 AA;

Query Match 55.4%; Score 806; DB 6; Length 281;
Best Local Similarity 55.2%; Pred. No. 2e-69;
Matches 153; Conservative 39; Mismatches 85; Indels 0; Gaps 0;

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Qy          1 MRRMTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEE 60
              :  : || || :| ||||||  || | :|  |:|||  |::|||||:|||||| ||  |
Db          5 LETVALPGGERVPKLGQGTWEMGERPAKRAAEIAALREGVDLGMTLIDTAEMYGDGATET 64

Qy         61 VAGEALAGRRDEAFVVSKVMPSHASRSGTIAACERSLKRLGTDRIDLYLLHWQGRYPLQD 120
              : |:|||  |:  |:||||:| |||| | :|||| :|||| |||:|||||||:|  || :
Db         65 LVGDALADVRERLFIVSKVLPHHASRGGVVAACEATLKRLRTDRVDLYLLHWRGSIPLAE 124

Qy        121 TVAAFHQLVEDGKIRYWGVSNFDHRALAELQDVPGTSGLTTDQVLYNLSRRGPEYDLLPW 180
              |:| |  | : ||||||||||||   :  |   | :  |||:||||:|||||:|||||
Db        125 TIAGFEALRDAGKIRYWGVSNFDVDDMEALVAEAGGAVCATDQILYNLARRGPEFDLLPW 184

Qy        181 CADHQLPVMAYSPIEQGRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSPQ 240
               |  ::| :|||||:  |:   | |:::|    |||   |||||| : ::  |||| | :
Db        185 LARREMPAIAYSPIDHMRLPKRTALDEIARERGVSPTRVALAWVLGQPNVLAIPKAGSVE 244

Qy        241 HVRDNATALDVELTREDLDALDRAFPPPSGPRPLEML 277
              |||||  |||: |  |:|  ||  |  | | ||||||
Db        245 HVRDNRAALDLVLGEEELARLDAQFKSPRGKRPLEML 281
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RESULT 1
US-09-252-991A-29664
; Sequence 29664, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29664
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29664

Query Match 55.8%; Score 812; DB 4; Length 352;
Best Local Similarity 56.8%; Pred. No. 4.6e-80;
Matches 158; Conservative 44; Mismatches 70; Indels 6; Gaps 4;

```
Qy          1 MRRMTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEE 60
              |: :||  |: :  :|||||  || || |  |||||  |:|||||:|||||||:||||:
Db         80 MKTLTLIDGQEVAAIGQGTWHIGEQPGERKREVAALREGIELGMTLIDTAEMYAEGGAED 139

Qy         61 VAGEALAGRRDEAFVVSKVMPSHASRSGTIAACERSLKRLGTDRIDLYLLHWQGRYPLQD 120
              | | |:||||:| |:|||| | :||| |  |||||||:||| : |||||||||||||::
Db        140 VVGAAIAGRREEVFLVSKVYPHNASRKGLPAACERSLRRLGCETIDLYLLHWQGRYPLEE 199

Qy        121 TVAAFHQLVEDGKIRYWGVSNFDHRALAELQDVPGTSGLTTDQVLYNLSRRGPEYDLLPW 180
              |: || :| : |||  |||||||   | :: :: | |   |:||:|||  || |||||||
Db        200 TIEAFERLRDQGKILRWGVSNFD---LGDMYELDG-SACATNQVMYNLEERGIEYDLLPW 255

Qy        181 CADHQLPVMAYSPIEQ-GRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSP 239
              | :  :||||| |: | ||:|    | ::||||  | |  ||||:| :  :  |||| :
Db        256 CQERGMPVMAYCPVGQGGRLLRHPALGEIAARHDASSAQVALAWLLEQ-GVIAIPKAVTS 314

Qy        240 QHVRDNATALDVELTREDLDALDRAFPPPSGPRPLEML 277
               |:| || | |:||: :|| |||:|||||:  | | ::
Db        315 AHIRQNAAAADLELSADDLRALDQAFPPPTRKRNLAIV 352
```

RESULT 2
US-09-489-039A-7896
; Sequence 7896, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7896
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7896

Query Match 47.2%; Score 686.5; DB 4; Length 324;
Best Local Similarity 48.9%; Pred. No. 2e-66;
Matches 139; Conservative 45; Mismatches 93; Indels 7; Gaps 3;

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Qy          1 MRRMTLPSGE--SIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGA 58
              | : |:  ||  ::| :| |||  ||   :|  |||||  |:: |:|::||||||||||
Db         41 MVKKTVRFGEQAAVPAIGLGTWYMGEHAAQRQQEVAALRVGIDHGLTVIDTAEMYADGGA 100

Qy         59 EEVAGEALAGRRDEAFVVSKVMPSHASRSGTIAACERSLKRLGTDRIDLYLLHWQGRYPL 118
              ||| |:|: | ||   :|||| | || ::    ||| ||:|| || :|:|||||:|  ||
Db        101 EEVVGQAIRGLRDRVVLVSKVYPWHAGKAAMHRACENSLRRLQTDYLDMYLLHWRGDIPL 160

Qy        119 QDTVAAFHQLVEDGKIRYWGVSNFDHRALAELQDVPGTSGLTTDQVLYNLSRRGPEYDLL 178
              |:|| |  :|| :|||| ||||| |   :  |          |:||||:|: || |||||
Db        161 QETVEAMEKLVAEGKIRRWGVSNLDTEDMQALWRTADGEHCATNQVLYHLASRGIEYDLL 220

Qy        179 PWCADHQLPVMAYSPIEQ-GRILD----DTTLNDVAARHSVSPAAAALAWVLRRDSLCTI 233
              |||  | |||||| |: | ||: |     : : ::|    :: |   ||||:|   :  |
Db        221 PWCQQHSLPVMAYCPLAQAGRLRDGLFQHSDIINMANARGITVAQLLLAWVIRHPGVLAI 280

Qy        234 PKASSPQHVRDNATALDVELTREDLDALDRAFPPPSGPRPLEML 277
              |||:| :||  || |||: |: |:|  ||| :|||     |:|:
Db        281 PKAASIEHVVQNAAALDIVLSGEELAQLDRLYPPPQRKTRLDMV 324
```

RESULT 1
A97604
probable oxidoreductase (PA0804) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: A97604
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58.
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97604
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87786.1; PID:g15157157; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_3682
A;Map position: circular chromosome
C;Superfamily: aldehyde reductase

Query Match 55.7%; Score 810; DB 2; Length 281;
Best Local Similarity 57.7%; Pred. No. 3.5e-62;
Matches 158; Conservative 35; Mismatches 81; Indels 0; Gaps 0;

```
Qy          4 MTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEEVAG 63
              :|||||  :| || |||  ||      ||: ::   ::|||||||||||||| :||| |
Db          8 VTLPSGNEVPALGLGTWNMGETRSSADDEIESIRKAIDLGMTLVDTAEMYADGRSEEVVG 67

Qy         64 EALAGRRDEAFVVSKVMPSHASRSGTIAACERSLKRLGTDRIDLYLLHWQGRYPLQDTVA 123
               |:|||||| |:|||| | :||  ||  |||||| ||||| ||||||||:| :|| :|||
Db         68 TAIAGRRDEVFLVSKVYPWNASARGTAEACERSLARLGTDHIDLYLLHWRGEHPLGETVA 127

Qy        124 AFHQLVEDGKIRYWGVSNFDHRALAELQDVPGTSGLTTDQVLYNLSRRGPEYDLLPWCAD 183
               || :|  |||| |||||||   : ||  ||       :|||||||||||: ||||| :
Db        128 AFERLKSDGKIGNWGVSNFDTDDMEELFTVPEGKNCAANQVLYNLSRRGPEFSLLPWCQE 187

Qy        184 HQLPVMAYSPIEQGRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSPQHVR 243
               | :|:||||||||||||| :  |  :|  :  :||  |||::| || :  |||::|   :
Db        188 HGVPLMAYSPIEQGRILKNHELIRIAKAYQATPAQLALAFLLDRDGVIAIPKSASVSRIV 247

Qy        244 DNATALDVELTREDLDALDRAFPPPSGPRPLEML 277
               :|  | |:|:| ||  ||| |||||:    ||||
Db        248 ENRGATDLEITEEDWTALDAAFPPPTRKTSLEML 281
```

RESULT 2
AB2826
aldo/keto reductase Atu2032 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C;Accession: AB2826
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelland, E.; Palmieri, A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey, S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2826
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43024.1; PID:g17740488; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2032
A;Map position: circular chromosome
C;Superfamily: aldehyde reductase

Query Match 55.7%; Score 810; DB 2; Length 281;
Best Local Similarity 57.7%; Pred. No. 3.5e-62;
Matches 158; Conservative 35; Mismatches 81; Indels 0; Gaps 0;

```
Qy          4 MTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEEVAG 63
              :|||||  :| || |||  ||      ||: ::   ::|||||||||||||| :||| |
Db          8 VTLPSGNEVPALGLGTWNMGETRSSADDEIESIRKAIDLGMTLVDTAEMYADGRSEEVVG 67

Qy         64 EALAGRRDEAFVVSKVMPSHASRSGTIAACERSLKRLGTDRIDLYLLHWQGRYPLQDTVA 123
               |:|||||| |:|||| | :||  ||  |||||| ||||| ||||||||:| :|| :|||
Db         68 TAIAGRRDEVFLVSKVYPWNASARGTAEACERSLARLGTDHIDLYLLHWRGEHPLGETVA 127

Qy        124 AFHQLVEDGKIRYWGVSNFDHRALAELQDVPGTSGLTTDQVLYNLSRRGPEYDLLPWCAD 183
              || :|  ||||  |||||||   : ||  ||       :||||||||||: ||||| :
Db        128 AFERLKSDGKIGNWGVSNFDTDDMEELFTVPEGKNCAANQVLYNLSRRGPEFSLLPWCQE 187

Qy        184 HQLPVMAYSPIEQGRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSPQHVR 243
              | :|:||||||||||||| :  |  :|  :  :||  |||::| || :  |||::|   :
Db        188 HGVPLMAYSPIEQGRILKNHELIRIAKAYQATPAQLALAFLLDRDGVIAIPKSASVSRIV 247

Qy        244 DNATALDVELTREDLDALDRAFPPPSGPRPLEML 277
              :|  | |:|:| ||  ||| |||||:    ||||
Db        248 ENRGATDLEITEEDWTALDAAFPPPTRKTSLEML 281
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